OM protein - protein search, using sw model

GenCore version 4.5

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Run on:     May 18, 2002, 05:12:35 ; Search time 42.56 Seconds
(without alignments)
239.268 Million cell updates/sec

Title:     us-09-719-748-2_copy_13_275
Perfect score:     1343
Sequence:     1 YDIGEELGSGQFAIVKKCRE............LVKETRKRLTIQEALRHPWI 263

Scoring table:     BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:     105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters:     105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :     SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1124 | 83.7 | 1431 | 1 | DAPK_HUMAN | P53355; homo sapien |
| 2 | 653.5 | 48.7 | 1176 | 1 | KML5_BOVIN | Q28824 bos taurus |
| 3 | 647.5 | 48.2 | 1906 | 1 | KML5_CHICK | P11799 gallus gall |
| 4 | 642.5 | 47.8 | 1914 | 1 | KML5_HUMAN | Q15746 homo sapien |
| 5 | 639 | 47.6 | 397 | 1 | S17A_RABIT | Q9gm70 oryctolagus |
| 6 | 638 | 47.4 | 414 | 1 | S17A_HUMAN | Q9ue5 homo sapien |
| 7 | 636.5 | 47.4 | 1147 | 1 | KML5_RABIT | P29294 oryctolagus |
| 8 | 625 | 46.5 | 372 | 1 | S17B_HUMAN | Q94768 homo sapien |
| 9 | 611.5 | 45.5 | 438 | 1 | KML5_SHEEP | O02827 ovis aries |
| 10 | 571.5 | 42.6 | 607 | 1 | KMLC_RABIT | P07313 oryctolagus |
| 11 | 570.5 | 42.5 | 609 | 1 | KMLC_RAT | P20689 rattus norv |
| 12 | 530.5 | 39.5 | 295 | 1 | KMLC_DICDI | P25523/dictyosteli |
| 13 | 509 | 37.9 | 473 | 1 | KCC4_HUMAN | Q16566 homo sapien |
| 14 | 506 | 37.7 | 474 | 1 | KCC4_RAT | P13234 rattus norv |
| 15 | 505 | 37.6 | 469 | 1 | KCC4_MOUSE | P08414 mus musculu |
| 16 | 500 | 37.2 | 3038 | 1 | TRIO_HUMAN | 075962 homo sapien |
| 17 | 495 | 36.9 | 533 | 1 | KCCD_RAT | P15791 rattus norv |
| 18 | 488 | 36.3 | 499 | 1 | KCCD_HUMAN | Q13557 homo sapien |
| 19 | 485 | 36.1 | 370 | 1 | KCC1_HUMAN | Q14012 homo sapien |
| 20 | 485 | 36.1 | 374 | 1 | KCC1_RAT | Q63450 rattus norv |
| 21 | 483.5 | 36.0 | 424 | 1 | KPSH_HUMAN | P11801 homo sapien |
| 22 | 483 | 36.0 | 542 | 1 | CDP3_ORYSA | Q63450 oryza satis |
| 23 | 480 | 35.7 | 533 | 1 | CDP2_ORYSA | P53684 oryza satis |
| 24 | 479.5 | 35.7 | 740 | 1 | DCK1_HUMAN | P53683 homo sapien |
| 25 | 478.5 | 35.6 | 433 | 1 | DCK1_RAT | O15075 rattus norv |
| 26 | 478.5 | 35.6 | 756 | 1 | DCK1_MOUSE | O08875 mus musculu |
| 27 | 475 | 35.4 | 478 | 1 | KCCA_RAT | Q9jlm8 rattus norv |
| 28 | 471 | 35.1 | 478 | 1 | KCCA_MOUSE | P11275 mus musculu |
| 29 | 469 | 34.9 | 527 | 1 | KCCG_RAT | P11798 rattus norv |
| 30 | 468 | 34.8 | 532 | 1 | CDPK_DAUCA | P11730 daucus caro |
| 31 | 468 | 34.8 | 610 | 1 | CDP1_ARATH | P28582 arabidopsis |
| 32 | 464 | 34.5 | 534 | 1 | CDP1_ORYSA | Q06850 oryza satis |
| 33 | 462 | 34.4 | 508 | 1 | CDPK_SOYBN | P53682 glycine max |
| 34 | 462 | 34.4 | 513 | 1 | CDP2_MAIZE | P49101 zea mays (m |
| 35 | 460 | 34.3 | 542 | 1 | KCCB_MOUSE | P28652 mus musculu |
| 36 | 459 | 34.2 | 335 | 1 | KCC1_SCHPO | Q9p712 schizosacch |
| 37 | 458 | 34.1 | 512 | 1 | KI10_ARATH | Q38997 arabidopsis |
| 38 | 457 | 34.1 | 542 | 1 | KCCB_RAT | P08413 rattus norv |
| 39 | 457 | 34.0 | 664 | 1 | KCCB_HUMAN | Q13554 homo sapien |
| 40 | 456.5 | 34.0 | 406 | 1 | KPBH_RAT | P13325 rattus norv |
| 41 | 452.5 | 33.7 | 406 | 1 | KPBH_HUMAN | P15735 homo sapien |
| 42 | 452 | 33.7 | 386 | 1 | KPBG_RABIT | P00518 oryctolagus |
| 43 | 450 | 33.5 | 909 | 1 | CSKP_RAT | P62915 rattus norv |
| 44 | 450 | 33.5 | 921 | 1 | CSKP_HUMAN | O14936 homo sapien |
| 45 | 450 | 33.5 | 924 | 1 | CSKP_MOUSE | 070589 mus musculu |

ALIGNMENTS

RESULT 1

DAPK_HUMAN

| ID | DAPK_HUMAN | STANDARD; | PRT; | 1431 AA. |

AC    P53355;
DT    01-OCT-1996 (Rel. 34, Created)
DT    01-NOV-1997 (Rel. 35, Last sequence update)
DT    16-OCT-2001 (Rel. 40, Last annotation update)
DE    Death-associated protein kinase 1 (EC 2.7.1.-) (DAP kinase 1).
GN    DAPK1 OR DAPK.
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX    NCBI_TaxID=9606;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=95129831; PubMed=7828849;
RA    Deiss L.P., Feinstein E., Berissi H., Cohen O., Kimchi A.;
RT    "Identification of a novel serine/threonine kinase and a novel 15-kD
RT    protein as potential mediators of the gamma interferon-induced cell
RT    death.";
RL    Genes Dev. 9:15-30(1995).
RN    [2]
RP    REVISIONS TO 164-171.
RA    Feinstein E.;
RL    Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
CC    -!- FUNCTION: INVOLVED IN MEDIATING INTERFERON-GAMMA-INDUCED CELL
CC        DEATH.
CC    -!- PTM: AUTOPHOSPHORYLATED.
CC    -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC    -!- SIMILARITY: CONTAINS 10 ANK REPEATS.
CC    -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC    --------------------------------------------------------------------------
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CC    or send an email to license@isb-sib.ch).
CC    --------------------------------------------------------------------------
DR    EMBL; X76104; CAA53712.1; -.
DR    HSSP; Q63450; 1A06.
DR    MIM; 600831; -.
DR    InterPro; IPR002110; ANK.
DR    InterPro; IPR000488; Death.
DR    InterPro; IPR000719; Euk_pkinase.
DR    InterPro; IPR002290; Ser_thr_pkinase.
DR    Pfam; PF00023; ank; 8.
DR    Pfam; PF00531; death; 1.
DR    Pfam; PF00069; pkinase; 1.
DR    SMART; SM00248; ANK; 7.
DR    SMART; SM00220; S_TKc; 1.
DR    PROSITE; PS50088; DEATH; 1.
DR    PROSITE; PS50297; ANK_REP_REGION; 1.
DR    PROSITE; PS50017; DEATH_DOMAIN; 1.

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DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Phosphorylation; Serine/threonine-protein kinase; Repeat; ANK repeat; Apoptosis.
KW   Transferase; ATP-binding; Calmodulin-binding;
FT   DOMAIN     13    266   PROTEIN KINASE.
FT   DOMAIN    267    334   CALMODULIN-BINDING.
FT   REPEAT    378    407   ANK 1.
FT   REPEAT    411    440   ANK 2.
FT   REPEAT    444    473   ANK 3.
FT   REPEAT    478    507   ANK 4.
FT   REPEAT    511    540   ANK 5.
FT   REPEAT    544    573   ANK 6.
FT   REPEAT    577    606   ANK 7.
FT   REPEAT    610    639   ANK 8.
FT   REPEAT    876    905   ANK 9.
FT   REPEAT   1163   1197   ANK 10.
FT   DOMAIN   1313   1397   DEATH.
FT   NP_BIND    19     27   ATP (BY SIMILARITY).
FT   BINDING    42     42   ATP (BY SIMILARITY).
FT   ACT_SITE  139    139   BY SIMILARITY.
FT   MUTAGEN    42     42   K->A: LOSS OF ACTIVITY.
SQ   SEQUENCE   1431 AA;   160017 MW;  9EE84811004A155B CRC64;
```

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Query Match     83.8%;   Score 1124;  DB 1;  Length 1431;
Best Local Similarity   79.5%;  Pred. No. 5.8e-65;
Matches  209;  Conservative  41;  Mismatches  13;  Indels  0;  Gaps  0;

Qy    1  YDIGEELGSSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRGVSREEIEREVSILRQVL   60
         || |||||||||||:||||||||||||:|||||||||| :::  |||||:|||||||:: :
Db   13  YDTGEELGSSGQFAVVKKCREKSTGLQYAAKFIKKRRTKSSRRGVSREDIEREVSILKEIQ   72

Qy   61  HHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQILDGVNYLHT  120
         | |||||| ||||||||: |:||| ||||||||| |||| ||||| |:|||| ||:||||
Db   73  HPNVITLHEVYENRTDVILIELVAGGELFDFLAEKESLTEEEATEFLKQILNGVYYLHS   132

Qy  121  KKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYE  180
         :: ||||||||||||||:|:|  :||||||||| |:| | ||||||||||||||||||||
Db  133  LQIAHFDLKPENIMLLDRNVPKRIKIIDFGLAHKIDFGNEFKNIFGTPEFVAPEIVNYE   192

Qy  181  PLGLEADMWSIGVITYILLSGASPFLGDTKQETIANITSVSIDFDEEFFSHTSELAKDFI  240
         |||||||||||||||||||||||||||||||||:||:: :  :::|: |:|||:|||||
Db  193  PLGLEADMWSIGVITYILLSGASPFLGDTKQETLANVSAVNVEFEDEYFSNTSALAKDFI   252

Qy  241  RKLLVKETRKRLTLQEALRHPWI  263
         |:|||:  :||:|:::|:|||||
Db  253  RRLLVKDPKKRMTIQDSLQHPWI  275
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RESULT 2
KMLS_BOVIN
ID   KMLS_BOVIN   STANDARD;   PRT;   1176 AA.
AC   Q28824;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update) (MLCK)
DE   Myosin light chain kinase, smooth muscle (EC 2.7.1.117) (MLCK)
DE   [Contains: Telokin].
GN   MYLK.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Stomach;
RX   MEDLINE=93201148; PubMed=1284247;
RA   Kobayashi H., Inoue A., Mikawa T., Kuwayama H., Hotta Y., Masaki T.,
RA   Ebashi S.;
RT   "Isolation of cDNA for bovine stomach 155 kDa protein exhibiting
RT   myosin light chain kinase activity.";
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RL   J. Biochem. 112:786-791(1992).
CC   -!- FUNCTION: CALCIUM/CALMODULIN-DEPENDENT ENZYME RESPONSIBLE FOR
CC       SMOOTH MUSCLE CONTRACTION VIA PHOSPHORYLATION OF A SPECIFIC SERINE
CC       IN THE N-TERMINUS OF MYOSIN LIGHT CHAINS (MLC), AN EVENT THAT
CC       FACILITATES MYOSIN INTERACTION WITH ACTIN FILAMENTS.
CC   -!- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC       light-chain] phosphate.
CC   -!- SUBUNIT: TELOKIN BINDS CALMODULIN.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS OF MLCK ARE PRODUCED BY
CC       ALTERNATIVE INITIATION; A NON-MUSCLE FORM (WHICH IS THE LONGEST
CC       FORM); A SMOOTH-MUSCLE FORM AND TELOKIN (A C-TERMINAL SECTION WITH
CC       NO CATALYTIC ACTIVITY).
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; S57131; AAB25794.1; -.
DR   HSSP; P56276; ITLK.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_C2.
DR   InterPro; IPR003600; Ig-like.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; Immunoglobulin domain; Repeat;
KW   ATP-binding; Phosphorylation; Calmodulin-binding;
KW   Alternative initiation.
FT   CHAIN       1   1176   MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE
FT                          ISOZYME.
FT   INIT_MET 1022   1022   TELOKIN.
FT   CHAIN    1022   1176   FOR TELOKIN.
FT   DOMAIN    100    291   16 X 12 AA TANDEM REPEATS.
FT   REPEAT    100    111   1.
FT   REPEAT    112    123   2.
FT   REPEAT    124    135   3 (INCOMPLETE).
FT   REPEAT    136    147   4.
FT   REPEAT    148    159   5.
FT   REPEAT    160    171   6.
FT   REPEAT    172    183   7.
FT   REPEAT    184    195   8.
FT   REPEAT    196    207   9.
FT   REPEAT    208    219   10.
FT   REPEAT    220    231   11.
FT   REPEAT    232    243   12.
FT   REPEAT    244    255   13.
FT   REPEAT    256    267   14.
FT   REPEAT    268    279   15.
FT   REPEAT    280    291   16.
FT   DOMAIN    603    693   FIBRONECTIN TYPE-III.
FT   DOMAIN    725    980   PROTEIN KINASE.
FT   DOMAIN    972   1035   CALMODULIN-BINDING.
FT   DOMAIN   1084   1151   IG-LIKE C2-TYPE DOMAIN.
FT   NP_BIND   731    739   ATP (BY SIMILARITY).
FT   BINDING   754    754   ATP (BY SIMILARITY).
FT   ACT_SITE  846    846   BY SIMILARITY.
```

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FT   DOMAIN       1171   1176   POLY-GLU.
SQ   SEQUENCE   1176 AA;  128824 MW;  F53DC6D4D42D4B97 CRC64;
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Query Match                48.7%;
Best Local Similarity      48.5%;  Score 653.5;  DB 1;  Length 1176;
                Conservative  48;  Pred. No. 7.8e-35;
Matches 128;    Conservative  48;  Mismatches  79;  Indels  9;  Gaps  3;
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Qy    1  YDIGEELGSSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVL   60
         |||| ||||||| | ||::||| |||| :||||| | :|
Db  725  YDIEERLGSSGKFGQVFRLVEKKTGKIWAGKFFKAYSAK------EKENIRQEISIMNCLH  778

Qy   61  HHNVITLHDVYENRTDVYHILELVSGGELFDFLAQKE-SLSEEEATSFIKQILDGVNYLH  119
         | ::| : :| ::| :||:|||:||||||| |:  :| :|:::|| :|||:|| || :|
Db  779  HPKLVQCVDAFEEKANIWVLEIVSGGELFERIIDEDFELTERECIKYMKQISEGVEYIH  838

Qy  120  TKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNY  179
         | :: |:||||||||  :     ||||||||||| :: ||| |::|||||||||||:|||
Db  839  KQGIVHLDLKPENIMCVNKT--GTRIKLIDFGLARRLENAGSLKVLFGTPEFVAPEVINY  896

Qy  180  EPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDPDEEFSHTSELAKDF  239
         ||:| : :||||||| |||:|| ||| || :|||||:||:: ||:::|  ::|:|||||
Db  897  EPIGYATDMWSIGVICYILVSGLSPFMGDNDNETLANVTSATWDFDDEAFDEISDDAKDF  956

Qy  240  IRKLLVKETRKRLTIQEALRHPWI  263
         | :||   :|:||   :|:|||||
Db  957  ISNLLKKDMKNRLNCTQCLQHPWL  980
```

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RESULT   3
ID    KMLS_CHICK    STANDARD;    PRT;    1906 AA.
AC    P11799; P19038;
DT    01-OCT-1989 (Rel. 12, Created)
DT    01-OCT-1996 (Rel. 34, Last sequence update)
DT    16-OCT-2001 (Rel. 40, Last annotation update)
DE    Myosin light chain kinase, smooth muscle and non-muscle isozymes
DE    (EC 2.7.1.117) (MLCK) (Contains: Telokin).
OS    Gallus gallus (Chicken).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC    Gallus.
OX    NCBI_TaxID=9031;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=96039976; PubMed=7589469;
RA    Watterson D.M., Collinge M., Lukas T.J., van Eldik L.J., Birukov K.G.,
RA    Stepanova O.V., Shirinsky V.P.;
RT    "Multiple gene products are produced from a novel protein kinase
RT    transcription region.";
RL    FEBS Lett. 373:217-220(1995).
RN    [2]
RP    SEQUENCE FROM N.A. (MLCK-210).
RX    MEDLINE=90192792; PubMed=2315320;
RA    Olson N.J., Pearson R.B., Needleman D.S., Hurwitz M.J., Kemp B.E.,
RA    Means A.R.;
RT    "Regulatory and structural motifs of chicken gizzard myosin light
RT    chain kinase.";
RL    Proc. Natl. Acad. Sci. U.S.A. 87:2284-2288(1990).
RN    [3]
RP    SEQUENCE OF 649-1906 FROM N.A., AND PARTIAL SEQUENCE.
RC    TISSUE=Fibroblast;
RX    MEDLINE=96036738; PubMed=2202734;
RA    Shoemaker M.O., Lau W., Shattuck R.L., Kwiatkowski A.P.,
RA    Matrisian P.E., Guerra-Santos L., Wilson E., Lukas T.J.,
RA    van Eldik L.J., Watterson D.M.;
RT    "Use of DNA sequence and mutant analyses and antisense
RT    oligodeoxynucleotides to examine the molecular basis of nonmuscle
RT    myosin light chain kinase autoinhibition, calmodulin recognition, and
RT    activity.";
RL    J. Cell Biol. 111:1107-1125(1990).
RN    [4]
RP    SEQUENCE OF 1259-1906 FROM N.A.
RC    TISSUE=Gizzard;
RX    MEDLINE=87157587; PubMed=3030394;
RA    Guerrero V. Jr., Russo M.A., Olson N.J., Putkey J.A., Means A.R.;
RT    "Domain organization of chicken gizzard myosin light chain kinase
RT    deduced from a cloned cDNA.";
RL    Biochemistry 25:8372-8381(1986).
RN    [5]
RP    SEQUENCE OF 1750-1906 FROM N.A. (TELOKIN).
RC    TISSUE=Gizzard;
RX    MEDLINE=93073972; PubMed=1444462;
RA    Yoshikai S., Ikebe M.;
RT    "Molecular cloning of the chicken gizzard telokin gene and cDNA.";
RL    Arch. Biochem. Biophys. 299:242-247(1992).
RN    [6]
RP    SEQUENCE OF 1750-1906 FROM N.A. (TELOKIN).
RX    MEDLINE=92236611; PubMed=1373815;
RA    Collinge M., Matrisian P.E., Zimmer W.E., Shattuck R.L., Lukas T.J.,
RA    van Eldik L.J., Watterson D.M.;
RT    "Structure and expression of a calcium-binding protein gene contained
RT    within a calmodulin-regulated protein kinase gene.";
RL    Mol. Cell. Biol. 12:2359-2371(1992).
CC    -!- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
CC        MYOSIN LIGHT CHAIN, WHICH LEADS TO THE FORMATION CALMODULIN/
CC        MLCK SIGNAL TRANSDUCTION COMPLEXES WHICH ALLOW SELECTIVE
CC        TRANSDUCTION OF CALCIUM SIGNALS.
CC    -!- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC        light-chain] phosphate.
CC    -!- ALTERNATIVE PRODUCTS: AT LEAST THREE ISOFORMS OF MLCK ARE PRODUCED
CC        BY ALTERNATIVE INITIATION. A NON-MUSCLE FORM (MLCK-210; WHICH IS
CC        THE LONGEST FORM); A SMOOTH-MUSCLE FORM (MLCK-108) AND TELOKIN (A
CC        C-TERMINAL SECTION WITH NO CATALYTIC ACTIVITY).
CC    -!- TISSUE SPECIFICITY: TELOKIN IS EXPRESSED IN GIZZARD, HEART, LUNG,
CC        INTESTINE, AND SKELETAL MUSCLE ALTHOUGH THE LEVELS OF THE
CC        EXPRESSION IN THE LATTER WERE MUCH LESS THAN THAT IN THE GIZZARD.
CC    -!- DOMAIN: TELOKIN BINDS CALMODULIN.
CC    -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC    -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC    -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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CC    -----------------------------------------------------------------------
DR    EMBL; X52876; CAA37056.1; -.
DR    EMBL; X52876; CAA37057.1; -.
DR    EMBL; X52876; CAA37058.1; -.
DR    EMBL; M31048; AAA49069.1; -.
DR    EMBL; M14953; AAA69964.1; -.
DR    EMBL; M96655; AAA49083.1; -.
DR    EMBL; M88283; AAA48647.1; -.
DR    EMBL; M88284; AAB53768.1; -.
DR    PIR; A25810; A25810.
DR    PIR; A37099; A37099.
DR    HSSP; P56276; 1ILK.
DR    InterPro; IPR000719; Euk_pkinase.
DR    InterPro; IPR003961; FN_III.
DR    InterPro; IPR003006; Ig_MHC.
DR    InterPro; IPR003598; Ig_C2.
DR    InterPro; IPR003600; Ig_like.
DR    InterPro; IPR002290; Ser_thr_pkinase.
DR    Pfam; PF00041; fn3; 1.
DR    Pfam; PF00047; ig; 9.
DR    Pfam; PF00069; Pkinase; 1.
DR    SMART; SM00060; FN3; 1.
DR    SMART; SM00409; IG; 1.
DR    SMART; SM00410; IG_like; 1.
DR    SMART; SM00408; IGc2; 8.
DR    SMART; SM00220; S_TKc; 1.
DR    PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
```

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DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW   ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;
KW   Alternative Initiation.
FT   CHAIN            1    1906
FT   CHAIN          935    1906       MYOSIN LIGHT CHAIN KINASE, NON-MUSCLE
FT                                    ISOZYME (MLCK-210).
FT   CHAIN          935    1906       MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE
FT                                    ISOZYME (MLCK-108).
FT   CHAIN         1750    1906       TELOKIN (MLCK-108).
FT   INIT_MET       935     935       FOR MLCK-108.
FT   INIT_MET      1750    1750       FOR TELOKIN.
FT   DOMAIN        1330    1400       FIBRONECTIN TYPE-III.
FT   DOMAIN        1453    1708       PROTEIN KINASE.
FT   DOMAIN        1809    1876       IG-LIKE C2-TYPE DOMAIN.
FT   NP_BIND       1459    1467       ATP (BY SIMILARITY).
FT   BINDING       1482    1482       ATP (BY SIMILARITY).
FT   ACT_SITE      1574    1574       BY SIMILARITY.
FT   DOMAIN        1716    1728       CALMODULIN AUTOINHIBITION (AM13) REGION
FT                                    (POTENTIAL).
FT   DOMAIN        1730    1749       CALMODULIN RECOGNITION (RS20) REGION
FT                                    (POTENTIAL).
FT   DOMAIN        1317    1364       MOTIF IA.
FT   DOMAIN        1385    1402       MOTIF IB.
FT   DOMAIN         660    1833       4 X REPEATS, MOTIF IIA.
FT   REPEAT         660     676       IIA-1.
FT   REPEAT         758     774       IIA-2.
FT   REPEAT        1107    1123       IIA-3.
FT   REPEAT        1817    1833       IIA-4.
FT   DOMAIN         693    1866       5 X REPEATS, MOTIF IIB.
FT   REPEAT         693     708       IIB-1.
FT   REPEAT         791     807       IIB-2.
FT   REPEAT        1140    1156       IIB-3.
FT   REPEAT        1281    1297       IIB-4.
FT   REPEAT        1851    1866       IIB-5.
FT   DOMAIN         970    1226       4 X REPEATS, MOTIF III.
FT   REPEAT         970     987       III-1.
FT   REPEAT         999    1016       III-2.
FT   REPEAT        1061    1078       III-3.
FT   REPEAT        1209    1226       III-4.
FT   DOMAIN        1700    1763       CALMODULIN-BINDING.
FT   DOMAIN        1896    1906       POLY-GLU.
FT   MOD_RES       1748    1748       PHOSPHORYLATION.
FT   MOD_RES       1762    1762       PHOSPHORYLATION.
FT   CONFLICT      1439    1439       R -> Q (IN REF. 4).
SQ   SEQUENCE      1906 AA;  210445 MW;  AD7D8A3B69EE3363 CRC64;

Query Match     48.2%;  Score 647.5;  DB 1;  Length 1906;
Best Local Similarity   48.1%;  Pred. No. 3.3e-34;
Matches  127;  Conservative  48;  Mismatches  80;  Indels  9;  Gaps  3;

Qy      1 YDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRGVSREIEREVSILRQVL 60
          :|:| | |||||: | :||||| | :|: |||| |:| | |:| | |||||||
Db   1453 YNIEERLGSGKFGQVFRLVEKKTGKVWAGKFKAYSAK-------EKENIRDEISIMNCLH 1506

Qy     61 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKE-SLSEEATSFIKQILDGVNYLH 119
          :|:| : |  ||: ::||||||:||||||||  ::| | :|: |||| |  |:|| :
Db   1507 HPKLVQCVDAFEEKANIVMVLEMVSGGELFERIIDEDFELTERECIKYMRQISEGVEYIH 1566

Qy    120 TKKIAHFDLKPENIMLLDKNIPIPHIKLIIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNY 179
          :|: ||||||||||| :||: |||||||||||| : | |  :| ||:|||||||||:::|
Db   1567 KQGIVHLDLKPENIMCVNKT--GTSIKLIDFGLARRLESAGSLKVLFGTPEFVAPEVINY 1624

Qy    180 EPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDF 239
          ||:| | ||||||| :|||| |:|||:||  ::|||| |  |:|||::: | || ||||
Db   1625 EPIGYETDMWSIGVICYILLVSGLSPFMGDNDNETLANVTSATWDFDDEAFDEISDDAKDF 1684

Qy    240 IRKLLVKETRKRLTIQEALRHPWI 263
          | :||:|:  |:|  | |:|||| 
Db   1685 ISNLLKKDMKKSRLNCTQCLQHPWL 1708
```

RESULT 4

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KMLS_HUMAN
ID   KMLS_HUMAN     STANDARD;      PRT;   1914 AA.
AC   Q15746; Q14844; Q16794; O95796; O95797; O95798; O95799; Q9UBG5;
AC   Q9UIT9;
DT   15-JUL-1998 (Rel. 36, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Myosin light chain kinase, smooth muscle and non-muscle isozymes
DE   (MLCK) [Contains: Telokin (Kinase related protein)
DE   (EC 2.7.1.117) (MLCK)
DE   (KRP)].
GN   MYLK OR MLCK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1)
RC   TISSUE=Umbilical vein endothelial cells;
RX   MEDLINE=97304466; PubMed=9160829;
RA   Garcia J.G.N., Lazar V.L., Gilbert-Mcclain L.I., Gallagher P.J.,
RA   Verin A.D.;
RT   "Myosin light chain kinase in endothelium: molecular cloning and
RT   regulation.";
RL   Am. J. Respir. Cell Mol. Biol. 16:489-494(1997).
RN   [2]
RP   REVISIONS.
RA   Birukov K.G., Garcia J.G.N.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS 2; 3A; 3B AND 4).
RC   TISSUE=Hippocampus;
RX   MEDLINE=99216419; PubMed=10198165;
RA   Lazar V.L., Garcia J.G.N.;
RT   "A single human myosin light chain kinase gene (MLCK; MYLK).";
RL   Genomics 57:256-267(1999).
RN   [4]
RP   REVISIONS TO ISOFORM 2.
RA   Birukov K.G., Garcia J.G.N.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 923-1914 FROM N.A.
RC   TISSUE=Hippocampus;
RX   MEDLINE=96121365; PubMed=8575746;
RA   Potier M.-C., Chelot E., Pekarsky Y., Gardiner K., Rossier J.,
RA   Turnell W.G.;
RT   "The human myosin light chain kinase (MLCK) from hippocampus:
RT   cloning, sequencing, expression, and localization to 3qcen-q21.";
RL   Genomics 29:562-570(1995).
RN   [6]
RP   SEQUENCE OF 1614-1914 FROM N.A.
RC   TISSUE=Lung, and Placenta;
RA   Watterson M.D.;
RL   Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE OF 1456-1914 FROM N.A.
RC   TISSUE=Placenta;
RA   Watterson M.D.;
RL   MEDLINE=20007838; PubMed=10536370;
RA   Shinsky V.P., Van Eldik L.J., Halech J.;
RT   "Analysis of the kinase-related protein gene found at human chromosome
RT   3q21 in a multi-gene cluster: organization, expression, alternative
RT   splicing and polymorphic marker.";
RL   J. Cell. Biochem. 75:481-491(1999).
CC   -!- FUNCTION: CALCIUM/CALMODULIN-DEPENDENT ENZYME RESPONSIBLE FOR
CC       SMOOTH MUSCLE CONTRACTION VIA PHOSPHORYLATION OF A SPECIFIC SERINE
CC       IN THE N-TERMINUS OF MYOSIN LIGHT CHAINS (MLC), AN EVENT THAT
CC       FACILITATES MYOSIN INTERACTION WITH ACTIN FILAMENTS. CENTRAL
CC       DETERMINANT IN THE DEVELOPMENT OF VASCULAR PERMEABILITY AND TISSUE
CC       EDEMA FORMATION. IN THE NERVOUS SYSTEM IT HAS BEEN SHOWN TO
CC       CONTROL THE GROWTH INITIATION OF ASTROCYTIC PROCESSES IN CULTURE
CC       AND TO PARTICIPATE IN TRANSMITTER RELEASE AT SYNAPSES FORMED
CC       BETWEEN CULTURED SYMPATHETIC GANGLION CELLS. CRITICAL PARTICIPANT
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CC       IN SIGNALING SEQUENCES THAT RESULT IN FIBROBLAST APOPTOSIS.
CC   -!- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC       light-chain] phosphate.
CC   -!- SUBUNIT: TELOKIN BINDS CALMODULIN.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; A NON-MUSCLE FORM (THE
CC       LONGEST FORM), A SMOOTH-MUSCLE FORM AND TELOKIN (A C-TERMINAL
CC       SECTION WITH NO CATALYTIC ACTIVITY); ARE PRODUCED BY ALTERNATIVE
CC       INITIATION.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST 6 ISOFORMS; 1 (SHOWN HERE), 2, 3A,
CC       3B, 4 AND DEL-1790; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES ARE
CC       EXPRESSED IN A WIDE VARIETY OF ADULT AND FETAL TISSUES AND IN
CC       CULTURED ENDOTHELIUM WITH QUALITATIVE EXPRESSION APPEARING TO BE
CC       NEITHER TISSUE- NOR DEVELOPMENT-SPECIFIC. NON-MUSCLE ISOFORM 2 IS
CC       THE DOMINANT SPLICE VARIANT EXPRESSED IN VARIOUS TISSUES. TELOKIN
CC       HAS BEEN FOUND IN A WIDE VARIETY OF ADULT AND FETAL TISSUES.
CC   -!- PTM: MLCK IS PROBABLY DOWN-REGULATED BY PHOSPHORYLATION.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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DR   EMBL; U48959; AAC18423.2; -.
DR   EMBL; AF069601; AAD15921.2; -.
DR   EMBL; AF069602; AAD15922.1; -.
DR   EMBL; AF069603; AAD15923.1; -.
DR   EMBL; AF069604; AAD15924.1; -.
DR   EMBL; X85337; CAA59685.1; -.
DR   EMBL; AF096771; AAD51380.1; JOINED.
DR   EMBL; AF096766; AAD51380.1; JOINED.
DR   EMBL; AF096767; AAD51380.1; JOINED.
DR   EMBL; AF096768; AAD51380.1; JOINED.
DR   EMBL; AF096769; AAD51380.1; JOINED.
DR   EMBL; AF096770; AAD51380.1; JOINED.
DR   EMBL; AF096774; AAD54018.1; -.
DR   EMBL; AF096771; AAD51381.1; JOINED.
DR   EMBL; AF096769; AAD51381.1; JOINED.
DR   EMBL; AF096770; AAD51381.1; JOINED.
DR   EMBL; X90870; CAA62378.1; -.
DR   HSSP; P56276; 1TLK.
DR   MIM; 600922; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003962; FnIII_repeat.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_C2.
DR   InterPro; IPR003599; Ig_like.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 8.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00014; FNTYPEIII.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00408; IGc2; 8.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW   ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;
KW   Alternative initiation; Alternative splicing.
FT   CHAIN         1       1914    MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE
FT                                 ISOZYME.
FT   CHAIN         923     1914    MYOSIN LIGHT CHAIN KINASE, NON-MUSCLE
FT                                 ISOZYME.
FT   CHAIN        1761     1914    TELOKIN.
FT   INIT_MET      923      923    FOR MYOSIN LIGHT CHAIN KINASE, SMOOTH-
FT                                 MUSCLE ISOZYME.
FT   INIT_MET     1761     1761    FOR TELOKIN.
FT   DOMAIN       1343     1413    FIBRONECTIN TYPE-III.
FT   DOMAIN       1464     1719    PROTEIN KINASE.
FT   DOMAIN       1711     1774    CALMODULIN-BINDING.
FT   DOMAIN       1824     1891    IG-LIKE C2-TYPE DOMAIN.
FT   NP_BIND      1470     1478    ATP (BY SIMILARITY).
FT   BINDING      1493     1493    ATP (BY SIMILARITY).
FT   ACT_SITE     1585     1585    BY SIMILARITY.
FT   DOMAIN       1906     1914    POLY-GLU.
FT   DOMAIN        868      895    5 X 28 AA APPROXIMATE TANDEM REPEATS.
FT   REPEAT        868      895    I-1.
FT   REPEAT        896      923    I-2.
FT   REPEAT        924      951    I-3.
FT   REPEAT        952      979    I-4.
FT   REPEAT        980      998    I-5 (INCOMPLETE).
FT   DOMAIN        999     1063    6 X 12 AA APPROXIMATE TANDEM REPEATS.
FT   REPEAT        999     1003    II-1 (INCOMPLETE).
FT   REPEAT       1004     1015    II-2.
FT   REPEAT       1016     1027    II-3.
FT   REPEAT       1028     1039    II-4.
FT   REPEAT       1040     1051    II-5.
FT   REPEAT       1052     1063    II-6.
FT   VARSPLIC      437      506    VSGIPKPEVAWFLEGTPVRRQEGSIEVYEDAGSHYLCLLKA
FT                                 RTRDSGTYSCTASNAQGVSCSWTLQVER -> G (IN
FT                                 ISOFORM 2 AND ISOFORM 3B).
FT   VARSPLIC     1433     1439    DEVEVSD -> MKWRCQT (IN ISOFORM 3A,
FT                                 ISOFORM 3B AND ISOFORM 4).
FT   VARSPLIC     1473     1546    GKFGQVFRLVEKKTRKVWAGKFKAYSAKEKENIRQEISIM
FT                                 NCLHHPKLVQCVDAFEEKANIVWLEIVSGGEL -> L
FT                                 (IN ISOFORM 4).
FT   VARSPLIC     1655     1705    MISSING (IN ISOFORM DEL-1790).
FT   VARSPLIC     1790     1790    MISSING (IN ISOFORM 3B).
FT   CONFLICT      933      933    V -> M (IN REF. 5).
FT   CONFLICT      963      963    S -> P (IN REF. 3; AAD15922).
FT   CONFLICT     1022     1022    P -> A (IN REF. 5).
FT   CONFLICT     1048     1050    KPM -> EAH (IN REF. 5).
FT   CONFLICT     1162     1162    P -> L (IN REF. 3; AAD15922 AND
FT                                 AAD15923).
FT   CONFLICT     1210     1210    L -> P (IN REF. 5).
FT   CONFLICT     1280     1280    E -> D (IN REF. 3; AAD15922 AND
FT                                 AAD15923).
FT   CONFLICT     1284     1284    M -> I (IN REF. 3; AAD15922, AAD15923 AND
FT                                 AAD15923).
FT   CONFLICT     1300     1300    A -> G (IN REF. 5).
FT   CONFLICT     1316     1316    L -> S (IN REF. 5).
FT   CONFLICT     1326     1326    T -> S (IN REF. 5).
FT   CONFLICT     1478     1478    V -> D (IN REF. 5).
FT   CONFLICT     1511     1511    S -> T (IN REF. 3; AAD15922 AND
FT                                 AAD15923).
FT   CONFLICT     1563     1563    I -> T (IN REF. 5).
FT   CONFLICT     1609     1609    A -> P (IN REF. 5).
FT   CONFLICT     1639     1639    G -> R (IN REF. 5).
FT   CONFLICT     1639     1640    GY -> D (IN REF. 3; AAD15922, AAD15923)
```

```
Query Match
Best Local Similarity   47.8%;                     Score 642.5;  DB 1;  Length 1914;
                        47.7%;  Pred. No. 6.8e-34;
Matches 126;  Conservative 49;  Mismatches 80;  Indels 9;  Gaps 3;

Qy     1  YDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRGVSREEIEREVSILRQVL   60
          |||| | | |:|  |:|| : ||| ||||||| |||:| |: |: |:|| |||||||||
Db  1464  YDIEEERLGSGKFGQVFRLVEKKTRKVWAGKFKRAYSAK----------EKENIRQEISIMNCLH 1517

Qy    61  HHNVITLLHDVENRTDVWHIIELVSGGELFDFLAQEE-SLSEEEATSPIKQILDGVNYLH  119
          |:::|  |:|::|  :  : :|||||||||: :|| |:  |:|   :| ||:|||| |:|
Db  1518  HPKLVQCVDAFEEKANIVWLEIVSGGELFERIIDEDPELTERECIKYMRQISEGVEYIH  1577

Qy   120  TKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNY  179
          | | ||:||||||||:|| :|  |: |||||||   ||:| ||:|| |||||||||:|||
Db  1578  KOGIVHDLKPENIMCVNKT-GTRIKLIDFGLARRLENAGSLKVLFGTPEFVAPEVINY  1635
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Qy  180 EPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSGYDFDDEEFFSHTSELAKDF 239
        |||||||||| |||||||||||||||||:||| :||||:|| |: ||||:|  :  ||||
Db 1636 EPIGYATDMWSIGVICYILVSGLSPFMGDNDETLANVTSATWDFDDEAFFDEISDDAKDF 1695

Qy  240 IRKLLVKETRKRLTIQEALRHPWI 263
        :||||||||||||||||||||:|||
Db 1696 ISNLLKKDMKNRLDCTQCLQHPWL 1719
```

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RESULT 5
ID   S17A_RABIT     STANDARD;      PRT;   397 AA.
AC   Q9GM70;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Serine/threonine kinase 17A (EC 2.7.1.-) (DAP kinase-related
DE   apoptosis-inducing protein kinase 1) (rDRAK1).
GN   STK17A OR DRAK1.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Osteoclast;
RX   MEDLINE=21276420; PubMed=11279167;
RA   Kojima H., Nemoto A., Uemura T., Honma R., Ogura M., Liu Y.-K.;
RT   "rDRAK1, a novel kinase related to apoptosis, is strongly expressed in
RT   active osteoclasts and induces apoptosis.";
RL   J. Biol. Chem. 276:19238-19243(2001).
CC   -!- FUNCTION: PHOSPHORYLATES THE MYOSIN LIGHT CHAIN (MLC) (BY
CC       SIMILARITY) AND IS INVOLVED IN OSTEOCLAST APOPTOSIS.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BONE MARROW AND IN LOWER
CC       LEVELS IN BRAIN, HEART, LUNG, LIVER AND KIDNEY.
CC   -!- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AB042195; BAB16111.1; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Phosphorylation; Nuclear protein; Apoptosis.
FT   DOMAIN       44    304       PROTEIN KINASE.
FT   NP_BIND      50     58       ATP (BY SIMILARITY).
FT   BINDING      73              ATP (BY SIMILARITY).
SQ   SEQUENCE   397 AA;   44462 MW;  589041E107F50097 CRC64;
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Query Match             47.6%;  Score 639;  DB 1;  Length 397;
Best Local Similarity   46.0%;  Pred. No. 2e-34;
Matches  122;  Conservative   64;  Mismatches  67;  Indels  12;  Gaps   6;

Qy    4 GEELGSGQFAIVKKCREKSTGLEYAAKFIKKROSRASRRGVS-REEIEREVSILRQVLHH 62
        |||| ||:|||||:  :|| :|:|||||||:: :|::|||:|:|  :  ||  |::|| |||
Db   47 GRELGRGKFAVVRKCIQKDSGKEPAAKFMRKR-----RKGQDCRMEIIHEIAVL-ELAQD 100
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Qy  239 FIRKLLVKETRKRLTIQEALRHPWI 263
        |:|||||| :|||||||||| :||:|
Db  280 FIRKLLVKKPEDRATAEEECLKHPWL 304
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Qy   63 N--VITLHDVYENRTDVVHILELVSGGELFD--FLAQKESLSEEEATSFIKQILLDGVNYL 118
        |  :||| |||| |||  ||::::|:| ||:|  ||:|::|| ||:| ||:: |||||: :|
Db  101 NPWVINLHEVYETSSEMLLVLEVAAGGELFDSDQCVADRDEAFNEKDVQRLMRQILEGVHFL 160

Qy  119 HTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEVVAPEIVN 178
        || |:| |||||| :|| |:||| | | |:||||| |::|||| ||:|| ||::|||||::
Db  161 HTHDVVHLDLKPQNILLTSES-PLGDIKIVDFGLSRIVNSEELREIMGTPEVVAPEILS 219

Qy  179 YEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDDEEFFSHTSELAKD 238
        ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db  220 YDPISMATDMWSIGVLTYVMLTGISPFLGDNKQETFLNISQMNLSYSEEEFDTVSESAVD 279
```

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RESULT 6
ID   S17A_HUMAN     STANDARD;      PRT;   414 AA.
AC   Q9UEE5;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Serine/threonine kinase 17A (EC 2.7.1.-) (DAP kinase-related
DE   apoptosis-inducing protein kinase 1).
GN   STK17A OR DRAK1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-90.
RC   TISSUE=Placenta, and Liver;
RX   MEDLINE=99003259; PubMed=9786912;
RA   Sanjo H., Kawai T., Akira S.;
RT   "DRAKs, novel serine/threonine kinases related to death-associated
RT   protein kinase that trigger apoptosis.";
RL   J. Biol. Chem. 273:29066-29071(1998).
CC   -!- FUNCTION: PHOSPHORYLATES THE MYOSIN LIGHT CHAIN (MLC) AS AN
CC       EXOGENOUS SUBSTRATE AND IS INVOLVED IN APOPTOTIC SIGNALING. THE C-
CC       TERMINAL REGION PLAYS AN IMPORTANT ROLE IN KINASE ACTIVITY AND FOR
CC       INITIATION OF APOPTOSIS.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PLACENTA AND IN LOWER
CC       LEVELS IN HEART, LUNG, SKELETAL MUSCLE, KIDNEY AND PANCREAS.
CC   -!- PTM: AUTOPHOSPHORYLATED.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AB011420; BAA34126.1; -.
DR   HSSP; P00518; 1PHK.
DR   MIM; 604726;
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Phosphorylation; Nuclear protein; Apoptosis.
FT   DOMAIN       61    321       PROTEIN KINASE.
FT   DOMAIN       33     37       POLY-PRO.
FT   NP_BIND      67     75       ATP (BY SIMILARITY).
FT   BINDING      90              ATP (BY SIMILARITY).
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```
FT   MUTAGEN        90     90       K->A; LOSS OF ACTIVITY.
SQ   SEQUENCE   414 AA;  46559 MW;  0C1402904382A1A CRC64;

Query Match             47.5%;  Score  638;  DB 1;  Length 414;
Best Local Similarity   46.0%;  Pred. No. 2.4e-34;
Matches  122;  Conservative  65;  Mismatches  66;  Indels  12;  Gaps  6;

Qy    4 GEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVS-REEIEREVSILRQVLHH 62
         | || | ||| | :|  || |:  | |:| : | ::  |||  :  :: |  |  |
Db   64 GRELGRGKFAVVRKCIKKDSGKEFAAKFMKR-----RKGQDCRMEIHEIAVL-ELAQD 117

Qy   63 N--VITLHDVYENRTDVVHILELVSGGELFD-FLAQKESLSEEEATSFIKQILDGVNYL 118
Db  118 NPWVINLHEVYETASEMLVLVEYAAGGEIFDQCVADRREAFKEKDVQRLMRQILEGVHFL 177

Qy  119 HTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVN 178
Db  178 HTRDVVHLDLKPQNILLTSES-PLGDIKIVDFGLSRILKNSEELREIMGTPEVVAPEILS 236

Qy  179 YEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKD 238
Db  237 YDPISMATDMWSIGVLITVVMLTGISPFLGNDKQETFLNISQMNLSYSEEEFDVLSESAVD 296

Qy  239 FIRKLLVKETRKRLTIQEALRHPWI 263
Db  297 FIRTLLVKKPEDRATAEECLKHPWL 321


RESULT 7
KMLS_RABIT

ID   KMLS_RABIT    STANDARD;      PRT;  1147 AA.
AC   P29294; Q28729;
DT   01-DEC-1992 (Rel. 24, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Myosin light chain kinase, smooth muscle (EC 2.7.1.117) (MLCK)
DE   [Contains: Telokin].
GN   MYLK.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Smooth muscle;
RX   MEDLINE=92084695; PubMed=1748667;
RA   Gallagher P.J., Herring B.P.;
RT   "The carboxyl terminus of the smooth muscle myosin light chain kinase
RT   is expressed as an independent protein, telokin.";
RL   J. Biol. Chem. 266:23945-23952(1991).
RN   [2]
RP   SEQUENCE OF 993-1147 FROM N.A. (TELOKIN).
RX   MEDLINE=92084694; PubMed=1748666;
RA   Gallagher P.J., Herring B.P., Griffin S.A., Stull J.T.;
RT   "Molecular characterization of a mammalian smooth muscle myosin light
RT   chain kinase.";
RL   J. Biol. Chem. 266:23936-23944(1991).
CC   -!- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
CC       MYOSIN LIGHT CHAIN.
CC   -!- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC       light-chain] phosphate.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST THREE ISOFORMS OF MLCK ARE PRODUCED
CC       BY ALTERNATIVE INITIATION, A NON-MUSCLE FORM (WHICH IS THE LONGEST
CC       FORM); A SMOOTH-MUSCLE FORM AND TELOKIN (A C-TERMINAL SECTION WITH
CC       NO CATALYTIC ACTIVITY).
CC   -!- DOMAIN: TELOKIN BINDS CALMODULIN.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
```

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DR   EMBL; M76233; AAA73093.1; -.
DR   EMBL; M76234; AAA31408.1; -.
DR   EMBL; M76181; AAA31409.1; -.
DR   PIR; A41675; A41675.
DR   HSSP; P56276; 1TLK.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 2.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW   ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;
KW   Alternative initiation.
FT   CHAIN         1   1147       MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE
FT   CHAIN         1   1147       ISOZYME.
FT   CHAIN       993   1147       TELOKIN.
FT   INIT_MET    993    993       FOR TELOKIN.
FT   DOMAIN      100    288       16 X 12 AA TANDEM REPEATS.
FT   REPEAT      100    111       1.
FT   REPEAT      112    123       2.
FT   REPEAT      124    132       3 (INCOMPLETE).
FT   REPEAT      133    144       4.
FT   REPEAT      145    156       5.
FT   REPEAT      157    168       6.
FT   REPEAT      169    180       7.
FT   REPEAT      181    192       8.
FT   REPEAT      193    204       9.
FT   REPEAT      205    216       10.
FT   REPEAT      217    228       11.
FT   REPEAT      229    240       12.
FT   REPEAT      241    252       13.
FT   REPEAT      253    264       14.
FT   REPEAT      265    276       15.
FT   REPEAT      277    288       16.
FT   DOMAIN      574    644       FIBRONECTIN TYPE-III.
FT   DOMAIN      696    951       PROTEIN KINASE.
FT   DOMAIN      943   1006       CALMODULIN-BINDING.
FT   DOMAIN     1056   1123       IG-LIKE C2-TYPE DOMAIN.
FT   NP_BIND     702    710       ATP (BY SIMILARITY).
FT   BINDING     725    725       ATP (BY SIMILARITY).
FT   ACT_SITE    817    817       BY SIMILARITY.
FT   DOMAIN     1138   1147       POLY-GLU.
FT   CONFLICT   1114   1114       C -> R (IN REF. 2).
SQ   SEQUENCE  1147 AA;  125719 MW;  F039E624C6E31024 CRC64;

Query Match             47.4%;  Score  636.5;  DB 1;  Length 1147;
Best Local Similarity   47.3%;  Pred. No. 9.4e-34;
Matches  125;  Conservative  48;  Mismatches  82;  Indels  9;  Gaps  3;

Qy    1 YDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSSREEIEREVSILRQVL 60
         ||| |||||| | |:| |:|   |  | |||||    | : ||| : |  :||   |:|
Db  696 YDIEERLGSGKFGQVFRLVERKTGKIWAGKFFKAYSAK------EKENIPAEIGIMNCLH 749

Qy   61 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKE-SLSEEEATSFIKQILDGVNYLH 119
```

Db   750 HPKLVQCVDAFEEKANIVMVLEIVSGGELFERIIDEDFELTERECIKYMRQISEGVEYIH 809
             | | ||||||| ||:|| ::  | ||| |||||:||
Db   810 KQGIVHLDLKPENIMCVNKT--GTRIKIIDFGLARRLENAGSLKVLFGTPEFVAPEVINY 867
Qy   120 TKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNY 179

Qy   180 EPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDF 239
             ||: |||||||||:|| |||| |||||: ||:||| :::||| ||||| ||||
Db   868 EPISYATDMWSIGVICYILVSGLSPFMGDNDNETLANVISATWDFDDEAFDEISDDAKDF 927

Qy   240 IRKLLVKETRKRLTIQEALRHPWI 263
             ||||:||||||| :|:|||
Db   928 ISNLLKKDMKNRLDCTQCLQHPWL 951

RESULT 8

ID   S17B_HUMAN     STANDARD;     PRT;   372 AA.
AC   O94768;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Serine/threonine kinase 17B (EC 2.7.1.-) (DAP kinase-related
DE   apoptosis-inducing protein kinase 2).
GN   STK17B OR DRAK2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-62.
RC   TISSUE=Placenta, and Liver;
RX   MEDLINE=99003259; PubMed=9786912;
RA   Sanjo H., Kawai T., Akira S.;
RT   "DRAKs, novel serine/threonine kinases related to death-associated
RT   protein kinase that trigger apoptosis.";
RL   J. Biol. Chem. 273:29066-29071(1998).
CC   -!- FUNCTION: PHOSPHORYLATES THE MYOSIN LIGHT CHAIN (MLC) AS AN
CC       EXOGENOUS SUBSTRATE AND IS INVOLVED IN APOPTOTIC SIGNALING. THE C-
CC       TERMINAL REGION PLAYS AN IMPORTANT ROLE IN KINASE ACTIVITY AND FOR
CC       INITIATION OF APOPTOSIS.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PLACENTA, LUNG, PANCREAS
CC       AND IN LOWER LEVELS IN HEART, BRAIN, LIVER, SKELETAL MUSCLE AND
CC       KIDNEY.
CC   -!- PTM: AUTOPHOSPHORYLATED.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR   EMBL; AB011421; BAA34127.1; -.
DR   HSSP; P00518; 1PHK.
DR   MIM; 604727; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Phosphorylation; Nuclear protein; Apoptosis.
FT   DOMAIN       33    293       PROTEIN KINASE.
FT   DOMAIN      308    311       POLY-SER.
FT   NP_BIND      39     47       ATP (BY SIMILARITY).
FT   BINDING      62     62       ATP (BY SIMILARITY).
FT   MUTAGEN      62     62       K-->A: LOSS OF ACTIVITY.
SQ   SEQUENCE   372 AA;  42344 MW;  7E69FFAED6DC1FF3 CRC64;

Query Match             46.5%;  Score 625;  DB 1;  Length 372;
Best Local Similarity   48.3%;  Pred. No. 1.5e-33;
Matches   127;  Conservative   46;  Mismatches   80;  Indels   10;  Gaps    5;

Qy     5 EELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVS-REETEREVSILRQVLH-H 62
            || |||||||| ||||| |||:|||||||||   ||:|| |:|    ||| :::|:
Db    37 KELGRGKFAVVRQCISKSTGQEYAAKFLKKR-----RRGQDCRAEILHEIAVLELAKSCP 91

Qy    63 NVITLHDVYENRTDVVHILELVSGGELFDFLAQK--ESLSEEEATSPIKQILDGVNYLHT 120
            ||| |||||||| |  || |||||| ||| ||     ||:||  ||| |||| ||
Db    92 RVINLHEVYENTSEIILILEYAAGGEIFSILCLPELAEMVSENDVIRILKQILEGVYYLHQ 151

Qy   121 KKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYE 180
            || |||||||||||||||| | |||||||||||| |||||||:|||||||||||  |||:
Db   152 NNIVHLDLKPQNI-LLSSIYPLGDIKIVDFGMSRKIGHACELREIMGTPEYLAPEILNYD 210

Qy   181 PLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDFI 240
            |: |||||||||||||| ||||||||||:|||||| ::||| ||||||||||| | |
Db   211 PITTATDMWNIGIIAYMLLTHTSPFVGEDNQETYLNISQVNVDYSEEFTSSVSQLATDFI 270

Qy   241 RKLLVKETRKRLTIQEALRHPWI 263
            : |||| ||| |:|| ||
Db   271 QSLIVKNPEKRPTAEICLSHSWL 293

RESULT 9

ID   KMLS_SHEEP     STANDARD;     PRT;   438 AA.
AC   O02827;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Myosin light chain kinase, smooth muscle (EC 2.7.1.117) (MLCK)
DE   [Contains: Telokin] (Fragment).
GN   MYLK.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96139839; PubMed=8569750;
RA   Pato M.D., Kerc E., Lye S.J.;
RT   "Phosphorylation and partial sequence of pregnant sheep myometrium
RT   myosin light chain kinase.";
RL   Mol. Cell. Biochem. 149:59-65(1995).
CC   -!- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
CC       MYOSIN LIGHT CHAIN.
CC   -!- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC       light-chain] phosphate.
CC   -!- DOMAIN: TELOKIN BINDS CALMODULIN.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
DR   EMBL; S80867; AAB50715.2; -.
DR   HSSP; P56276; 1TLK.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_C2.

```
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00069; Pkinase; 1.
DR   SMART; SM00408; IG2; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; PARTIAL.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW   ATP-binding; Phosphorylation; Immunoglobulin domain.
FT   NON_TER       1
FT   DOMAIN      241              PROTEIN KINASE.
FT   DOMAIN      233    296       CALMODULIN-BINDING.
FT   DOMAIN      346    413       IG-LIKE C2-TYPE DOMAIN.
FT   BINDING      15              ATP (BY SIMILARITY).
FT   BINDING      15              BY SIMILARITY.
FT   ACT_SITE    107              BY SIMILARITY.
FT   DOMAIN      283    438       TELOKIN.
FT   DOMAIN      433    438       POLY-GLU.
SQ   SEQUENCE    438 AA;  49503 MW;  77A02F4885A10B51 CRC64;

Query Match    45.5%;  Score 611.5;  DB 1;  Length 438;
Best Local Similarity   48.2%;  Pred. No. 1.3e-32;
Matches 118;  Conservative 46;  Mismatches 72;  Indels 9;  Gaps 3;

Qy    20  EKSTGLEYAAKFIKKRQSRASRGVSREEIEREVSILRQVLHHNVITLHDVYENRTDVVH 79
              :: ||  | ||: |  ::|||::|:| ::: || | ||||::|||:||  |:  :
Db     5  EKRTGVWAGKFPKAYSAK------EKENIRQEISIMNCLHHPKLVQCVDAFEEKANIVM 58

Qy    80  ILELVSGGELFDFLAQKE-SLSEEEATSFIKQILDGVNLHTKIAHFDLKPENIMLLDK 138
          :||:||||||| : : ::  : :: || :::  : :: | |   :|:|||||||| :||
Db    59  VLEIVSGGELFERIIDEDPELTERECIKYMKQISEGVETIHKQGTVHLDLKPENIMCVNK 118

Qy   139  NIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYEPLGLEADMWSIGVITYIL 198
            | | |||||||||:: |:|  :| |:||:||||||:|||||:| : ||||||||| |||
Db   119  T--GTRIKLIDFGLARRLENAGSLKVLFGSTPEFVAPEVINYEPIGYATDMWSIGVICYIL 176

Qy   199  LSGASPFLGDTKQETLANITSVSVDFDEEFFSHTSELAKDFIRKLLVKETRKRLTIQEAL 258
          :||:||| || :|:|||:|:|  ::|||: | ||:| ||||| ::|:|  : |||  ::|
Db   177  VSGLSPFMGDNDNETLANVTSATWDFDDEAFDEISDDAKDFISNLLKKDIKNRLNCTQCL 236

Qy   259  RHPWI 263
          :|||:
Db   237  QHPWL 241

RESULT 10
KMLC_RABIT   STANDARD;   PRT;   607 AA.
ID   KMLC_RABIT
AC   P07313;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Myosin light chain kinase, skeletal muscle (EC 2.7.1.117) (MLCK).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90112242; PubMed=1688558;
RA   Herring B.P., Stull J.T., Gallagher P.J.;
RT   "Domain characterization of rabbit skeletal muscle myosin light chain
RT   kinase.";
RL   J. Biol. Chem. 265:1724-1730(1990).
RN   [2]
RP   SEQUENCE OF 1-603.
RX   MEDLINE=87101105; PubMed=3542042;
RA   Takio K., Blumenthal D.K., Walsh K.A., Titani K., Krebs E.G.;
RT   "Amino acid sequence of rabbit skeletal muscle myosin light chain
RT   kinase.";
RL   Biochemistry 25:8049-8057(1986).
RN   [3]
```

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RP   SEQUENCE OF 295-603.
RX   MEDLINE=86104095; PubMed=3841288;
RA   Takio K., Blumenthal D.K., Edelman A.M., Walsh K.A., Krebs E.G.,
RA   Titani K.;
RT   "Amino acid sequence of an active fragment of rabbit skeletal muscle
RT   myosin light chain kinase.";
RL   Biochemistry 24:6028-6037(1985).
RN   [4]
RP   STRUCTURE BY NMR OF 577-602.
RX   MEDLINE=92263094; PubMed=1585175;
RA   Ikura M., Clore G.M., Gronenborn A.M., Zhu G., Klee C.B., Bax A.;
RT   "Solution structure of a calmodulin-target peptide complex by
RT   multidimensional NMR.";
RL   Science 256:632-638(1992).
-!-  FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
CC       MYOSIN LIGHT CHAIN.
-!-  CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC       light-chain] phosphate.
-!-  SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
```

```
DR   EMBL; J05194; AAA31400.1; -.
DR   PIR; A25830; A25830.
DR   PIR; A05120; A05120.
DR   PIR; A35021; A35021.
DR   PDB; 2BBM; 31-JAN-94.
DR   PDB; 2BBN; 31-JAN-94.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW   ATP-binding; Phosphorylation; Acetylation; 3D-structure.
FT   INIT_MET      0      0
FT   MOD_RES       1      1       ACETYLATION.
FT   DOMAIN      296                PROTEIN KINASE.
FT   DOMAIN      585    551       CALMODULIN-BINDING.
FT   DOMAIN             597       PROTEIN KINASE.
FT   NP_BIND     302    310       ATP (BY SIMILARITY).
FT   BINDING     325    325       ATP (BY SIMILARITY).
FT   ACT_SITE    417    417       BY SIMILARITY.
FT   CONFLICT    335    335       K -> KK (IN REF. 2 AND 3).
FT   HELIX       581    595
FT   HELIX       596    595
FT   TURN        596    596
SQ   SEQUENCE    607 AA;  65337 MW;  6E67764175lA04C8 CRC64;

Query Match   42.6%;  Score 571.5;  DB 1;  Length 607;
Best Local Similarity   43.1%;  Pred. No. 6.9e-30;
Matches 112;  Conservative 54;  Mismatches 85;  Indels 9;  Gaps 3;

Qy     5  EELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRGVSREEIEREVSILRQVLHHNV 64
          | |||| | :|      ||||  ||| || |::                 ||||:|:||:|
Db   300  EALGGKFGAVCTCTEKSTGLKLAAKVIKQTPK----------DKEMVMLEIEVMNQLNHNL 353

Qy    65  ITLHDVYENRTDVVHILELVSGGELFDFLAQKE-SLSEEEATSFIKQILDGVNLHTKI 123
           : :  :|   |:| : | |||||||| ::  ::     |  : :|: : ||:|: |  :
Db   354  IQIYAAIETPHEIVLFMEYIEGGELFERIVDEDYHLTEVDTMVFVRQICDGILFMHKRV 413

Qy   124  AHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYEPLG 183
           |:||||||: | | :::  :|||||||||  :  :  :|  ||||||| :||:|||: :
Db   414  LHDLKPENILCVNTTGHL--VKIIDFGLARRYNPKEKLKVNFGTPEFLSPEVVNYDQIS 471

Qy   184  LEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSVDFDEEFFSHTSELAKDFIRKL 243
```

Db  472  DKTDMWSLGVITYMLLSGLSPFLGDDDTETLNNVLSGNWYFDEETFEAVSDEAKDFVSNL 531
         |||||||||||||||||||||:||||||:|:|||||: :| :|||:|:
Qy  244  LVKETRKRLTIQEALRHPWI 263
         |:|: |||| ||
Db  532  IVKEQGARMSAAQCLAHPWL 551

Qy  532  IVKEQGARMSAAQCLAHPWL 551

RESULT 11

ID   KMLC_RAT         STANDARD;      PRT;    609 AA.
AC   P20689;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Myosin light chain kinase, skeletal muscle (EC 2.7.1.117) (MLCK).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88273159; PubMed=2839493;
RA   Roush C.L., Kennelly P.J., Glaccum M.B., Helfman D.M., Scott J.D.,
RA   Krebs E.G.;
RT   "Isolation of the cDNA encoding rat skeletal muscle myosin light
RT   chain kinase. Sequence and tissue distribution.";
RL   J. Biol. Chem. 263:10510-10516(1988).
CC   -!- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
CC       MYOSIN LIGHT CHAIN.
CC   -!- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC       light-chain] phosphate.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       --------------------------------------------------------------------------
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CC       entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC       or send an email to license@isb-sib.ch).
CC       --------------------------------------------------------------------------
DR   EMBL; J03886; AAA41625.1; ALT_SEQ.
DR   PIR; A28798; A28798.
DR   HSSP; P00518; 1PHK.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW   ATP-binding; Phosphorylation; Acetylation.
FT   INIT_MET      0      0
FT   MOD_RES       1      1       ACETYLATION (BY SIMILARITY).
FT   DOMAIN      298    553       PROTEIN KINASE.
FT   DOMAIN      587    599       CALMODULIN-BINDING (BY SIMILARITY).
FT   NP_BIND     304    312       ATP (BY SIMILARITY).
FT   BINDING     327    327       ATP (BY SIMILARITY).
FT   ACT_SITE    419    419       BY SIMILARITY.
SQ   SEQUENCE   609 AA;  65685 MW;  0073A22659BD1358 CRC64;

Query Match             42.5%;  Score 570.5;  DB 1;  Length 609;
Best Local Similarity   41.5%;  Pred. No. 8e-30;
Matches  108;  Conservative  58;  Mismatches  85;  Indels  9;  Gaps  3;

Qy     5  EELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVLHHHV  64
          || |: ||||||||||| | ||:||||:||:||  :| |:||::||||:|||: :|
Db   302  EALGGGKFGAVCTCTERSTGLKLAAKVIKKQTPK-----DKEMVLLEIEVMNQLNHRNL 355

Qy    65  ITLHDYVENRTDVHILELVSGGELFDFLAQKE-SLSEEEATSFIKQILDGVNYLHTKKI 123

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DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Phosphorylation.
FT   DOMAIN        8    265       PROTEIN KINASE.
FT   DOMAIN      264    295       AUTOINHIBITORY DOMAIN.
FT   DOMAIN       14     22       PROTEIN.
FT   NP_BIND      37     37       ATP (BY SIMILARITY).
FT   BINDING     130    130       ATP (BY SIMILARITY).
FT   ACT_SITE    130    130       BY SIMILARITY.
SQ   SEQUENCE   295 AA;  33406 MW;  546CAEDB8F6ECD0B CRC64;
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Query Match    39.5%;  Score 530.5;  DB 1;  Length 295;
Best Local Similarity  43.6%;  Pred. No. 1.3e-27;
Matches  115;  Conservative  41;  Mismatches  101;  Indels  7;  Gaps  3;

Qy    1  YDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREE-IEREVSILRQV   59
Db    8  YEFKEELGRGAFSIVLGENKQTKQRYAIKVINK----SELGKDYEKNIKMEVDILKKV    62

Qy   60  LHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQILDGVNYLH  119
Db   63  NHPNIIALKELFDTPEKLYLVMELVTGGELFDKIVEKGSYSEADAANLVKKIVSAVGYLH  122

Qy  120  TKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNY  179
Db  123  GLNIVHRDLKPENLLLKSKENHL-EVAIADFGLSKIIGCQTLVMQTACGTPSYVAPEVLNA 181

Qy  180  EPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDF  239
Db  182  TGVDKEVDMWSIGVITYILLCGFPPFYGDTVPEIFEQIMEANYEFPEEYWGGISKEAKDF  241

Qy  240  IRKLLVKETRKRLTIQEALRHPWI  263
Db  242  IGKLLVVDVSKRLNATNALNHPWL  265
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RESULT 13
KCC4_HUMAN
ID   KCC4_HUMAN     STANDARD;    PRT;    473 AA.
AC   Q16566;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Calcium/calmodulin-dependent protein kinase type IV catalytic chain
DE   (EC 2.7.1.123) (CAM kinase-GR) (CaMK IV) [Contains: Calspermin].
GN   CAMK4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94375404; PubMed=8089075;
RA   Kitani T., Okuno S., Fujisawa H.;
RT   "cDNA cloning and expression of human calmodulin-dependent protein
RT   kinase IV.";
RL   J. Biochem. 115:637-640(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94252566; PubMed=8194751;
RA   Bland M.M., Monroe R.S., Ohmstede C.A.;
RT   "The cDNA sequence and characterization of the
RT   Ca2+/calmodulin-dependent protein kinase-Gr from human brain and
RT   thymus.";
RL   Gene 142:191-197(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
```

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RC   TISSUE=Blood;
RX   MEDLINE=94199862; PubMed=8107230;
RA   Mosialos G., Hanissian S.H., Jawahar S., Vara L., Kieff E.,
RA   Chatila T.A.;
RT   "A Ca2+/calmodulin-dependent protein kinase, Cam kinase-Gr, expressed
RT   after transformation of primary human B lymphocytes by Epstein-Barr
RT   virus (EBV) is induced by the EBV oncogene LMP1.";
RL   J. Virol. 68:1697-1705(1994).
-!-  FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
-!-     PROTEIN.
-!-  CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
-!-  SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL
-!-     NUCLEI (BY SIMILARITY).
-!-  ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE
-!-     TYPE IV CATALYTIC CHAIN AND CALSPERMIN ARE OBTAINED BY ALTERNATIVE
-!-     SPLICING.
-!-  SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
-!-     CAMK SUBFAMILY.
```

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DR   EMBL; D30742; BAA06403.1; -.
DR   EMBL; L70000; AAA35639.1; -.
DR   EMBL; L24959; AAA18251.1; -.
DR   HSSP; Q63450; 1A06.
MIM; 114080; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Calmodulin-binding; Alternative splicing; CALSPERMIN.
FT   CHAIN         1    473       PROTEIN KINASE.
FT   DOMAIN       46    300       PROTEIN KINASE.
FT   NP_BIND      52     60       ATP (BY SIMILARITY).
FT   BINDING      75     75       ATP (BY SIMILARITY).
FT   ACT_SITE    164    164       BY SIMILARITY.
FT   DOMAIN      322    341       CALMODULIN-BINDING (POTENTIAL).
SQ   SEQUENCE   473 AA;  51925 MW;  EFEE51E5612326DC CRC64;
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Query Match    37.9%;  Score 509;  DB 1;  Length 473;
Best Local Similarity  40.7%;  Pred. No. 5.4e-26;
Matches  109;  Conservative  49;  Mismatches  92;  Indels  18;  Gaps  5;

Qy    1  YDIGEELGSGQFAIVKKCCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVL   60
Db   46  FEVESELGRGATSIVYRCKQKGTQKPYALKVLKKT------VDKKIVRTEIGVLLRLS    97

Qy   61  HHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQILDGVNYLHT  120
Db   98  HPNIKLKEIFETPTEISLVELVTGGELFDRIVEKGYYSERDAADAVKQILEAVAYLHE   157

Qy  121  KKIAHFDLKPENIMLLDKNIPIPH--IKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVN  178
Db  158  NGIVHRDLKPENLLYA---TPAPDAPIKIADFGLSKIVEHQVLMKTVCGTPGYCAPEILR  214

Qy  179  YEPLGLEADMWSIGVITYILLSGASPFL---GDTKQETLANITSVSYDFDEEFFSHTSEL  235
Db  215  GCAYGPEVDMWSVGIITYILLCGFPEFYDERGD--QEMFRRILNCEYFISPWWDEVSLN  272

Qy  236  AKDFIRKLLVKETRKRLTIQEALRHPWI  263
Db  273  AKDLVRKLIVLDPKKRLTTFQALQHPWV  300
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RESULT 14
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ID   KCC4_RAT      STANDARD;     PRT;  474 AA.
AC   P13234;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Calcium/calmodulin-dependent protein kinase type IV catalytic chain
DE   (EC 2.7.1.123) (CAM Kinase-GR) (CaMK IV) [Contains: Calspermin].
GN   CAMK4.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX   MEDLINE=91285548; PubMed=1648230;
RA   Ohmstede C.-A., Bland M.M., Merrill B.M., Sahyoun N.;
RT   "Relationship of genes encoding Ca2+/calmodulin-dependent protein
RT   kinase Gr and calspermin to a gene within a gene.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:5784-5788(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91304387; PubMed=1649385;
RA   Means A.R., Cruzalegui F., Lemagueresse B., Needleman D.S.,
RA   Slaughter G.R., Ono T.;
RT   "A novel Ca2+/calmodulin-dependent protein kinase and a male germ
RT   cell-specific calmodulin-binding protein are derived from the same
RT   gene.";
RL   Mol. Cell. Biol. 11:3960-3971(1991).
RN   [3]
RP   SEQUENCE OF 250-474 FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX   MEDLINE=89174647; PubMed=2538431;
RA   Ohmstede C.-A., Jenson K.F., Sahyoun N.;
RT   "Ca2+/calmodulin-dependent protein kinase enriched in cerebellar
RT   granule cells. Identification of a novel neuronal
RT   calmodulin-dependent protein kinase.";
RL   J. Biol. Chem. 264:5866-5875(1989).
RN   [4]
RP   SEQUENCE OF 306-474 FROM N.A. AND SEQUENCE OF 335-361.
RC   STRAIN=SPRAGUE-DAWLEY;
RX   MEDLINE=89123272; PubMed=2914893;
RA   Ono T., Slaughter G.R., Cook R.G., Means A.R.;
RT   "Molecular cloning sequence and distribution of rat calspermin, a
RT   high affinity calmodulin-binding protein.";
RL   J. Biol. Chem. 264:2081-2087(1989).
CC   -!- FUNCTION: CAM KINASE GR IS A NEURONAL-SPECIFIC PROTEIN KINASE,
CC       ENRICHED IN CEREBELLAR GRANULE CELLS.
CC   -!- FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
CC       PROTEIN.
CC   -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC   -!- ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE
CC       TYPE IV CATALYTIC CHAIN AND CALSPERMIN ARE OBTAINED BY ALTERNATIVE
CC       SPLICING.
CC   -!- TISSUE SPECIFICITY: CALSPERMIN IS PREDOMINANTLY FOUND IN MAMMALIAN
CC       TESTIS AND BRAIN.
CC   -!- PTM: THE N-TERMINAL OF CALSPERMIN IS BLOCKED.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   -!- SIMILARITY: CAMK SUBFAMILY.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; M63334; AAA40865.1; -.
DR   EMBL; M74488; AAA40845.1; ALT_SEQ.
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DR   EMBL; M64757; AAA40856.1; -.
DR   EMBL; M64757; AAA40857.1; -.
DR   EMBL; J04600; AAA41867.1; -.
DR   EMBL; J04446; AAA40990.1; -.
DR   PIR; A41103; TVRIC4.
DR   HSSP; P00518; 1PHK.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; Alternative splicing;
KW   Calmodulin-binding; Testis; ATP-binding.
FT   CHAIN        1    306       PROTEIN KINASE.
FT   CHAIN       42    474       CALSPERMIN.
FT   DOMAIN      46    296       PROTEIN KINASE.
FT   NP_BIND     48     56       ATP (BY SIMILARITY).
FT   BINDING     71     71       ATP (BY SIMILARITY).
FT   ACT_SITE   160    160       BY SIMILARITY.
FT   DOMAIN     318    337       CALMODULIN-BINDING (POTENTIAL).
FT   DOMAIN     393    399       POLY-GLU.
FT   DOMAIN     403    413       POLY-GLU.
FT   CONFLICT   372    372       I -> M (IN REF. 2 AND 4).
SQ   SEQUENCE   474 AA;  53133 MW;  56F71AC5644DED23 CRC64;
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Query Match    37.7%;  Score 506;  DB 1;  Length 474;
Best Local Similarity   40.3%;  Pred. No. 8.5e-26;
Matches 108; Conservative 50; Mismatches 92; Indels 18; Gaps 5;

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Qy     1 YDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVL  60
         ::|: :|||| :: || ||  :||| || :|   : ||  | :| : : : |  : : :
Db    42 FEVESELGRGATSIVYRCKQKGTQKPYALKVLKKT---------VDKKIVRTEIGVLLRLS  93

Qy    61 HHNVITLHDVYENRTDVVHILELVSGGELFDRIVEKGYYSEED  120
         |:|:|  |||:|    |::||| :|||||||||| : | |
Db    94 HPNIIKLKEIFETPTEISLVLELVTGGELFDRIVEKGYYSERDAADAVKQILEAVAYLHE  153

Qy   121 KKIAHFDLKPENIMLLDKNIPIPH---IKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVN  178
         :|:||||||||::|   |:|  :    ||||||||  |: |||| |   ||||| | | :
Db   154 NGIVHRDLKPENLLYA---TPAPDAPLKIADFGLSKIVEHQVLMKTVCGTPGYCAPEILR  210

Qy   179 YEPLGLEADMWSIGVITYILLSGASPFL---GDTKQETLANITSVSYDFDEEFFSHTSEL  235
         |  | | ||||:||||| |  ||  ||     | |||||   |  | :     |||
Db   211 GCAYGPEVDMWSVGIITYILLCGFEPFYDERGD--QFMFRRILNCEYYFISPWWDEVSLN  268

Qy   236 AKDFIRKLLVKETRKRLTIQEALRHPWI  263
         |||: :||||: |  |||:  | |||
Db   269 AKDLVKKLIVLDPKKRLTTFQALQHPWV  296
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RESULT 15
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ID   KCC4_MOUSE    STANDARD;     PRT;  469 AA.
AC   P08414; Q61381;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Calcium/calmodulin-dependent protein kinase type IV catalytic chain
DE   (EC 2.7.1.123) (CAM Kinase-GR) (CaMK IV) [Contains: Calspermin].
GN   CAMK4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=Brain;
RX   MEDLINE=91372388; PubMed=1893997;
RA   Jones D.A., Glod J., Wilson-Shaw D., Hahn W.E., Sikela J.M.;
RT   "cDNA sequence and differential expression of the mouse
RT   Ca2+/calmodulin-dependent protein kinase IV gene.";
```

RL   FEBS Lett. 289:105-109(1991).
RN   [2]
RP   SEQUENCE OF 240-469 FROM N.A.
RX   MEDLINE=89122027; PubMed=2536634;
RA   Sikela J.M., Law M.L., Kao F.-T., Hartz J.A., Wei Q., Hahn W.E.;
RT   "Chromosomal localization of the human gene for brain
RT   Ca2+/calmodulin-dependent protein kinase type IV.";
RL   Genomics 4:21-27(1989).
RN   [3]
RP   SEQUENCE OF 315-469 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=87204263; PubMed=3033675;
RA   Sikela J.M., Hahn W.E.;
RT   "Screening an expression library with a ligand probe: isolation and
RT   sequence of a cDNA corresponding to a brain calmodulin-binding
RT   protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:3038-3042(1987).
CC   -!- FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
CC       PROTEIN.
CC   -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC   -!- SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL
CC       NUCLEI.
CC   -!- ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE
CC       TYPE IV CATALYTIC CHAIN AND CALSPERMIN ARE OBTAINED BY ALTERNATIVE
CC       SPLICING.
CC   -!- TISSUE SPECIFICITY: BRAIN AND TESTIS.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       CAMK SUBFAMILY.
CC   --------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M16206; AAA39933.1; -.
DR   EMBL; M64266; AAA37364.1; -.
DR   EMBL; J03057; AAA37366.1; -.
DR   EMBL; X58995; CAA41741.1; -.
DR   PIR; A29878; A29878.
DR   PIR; S17656; S17656.
DR   HSSP; Q63350; 1A06.
DR   MGD; MGI:88258; Camk4.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Calmodulin-binding; Alternative splicing.
FT   CHAIN         1    469       CALSPERMIN.
FT   DOMAIN       46    306       PROTEIN KINASE.
FT   NP_BIND      52     56       ATP (BY SIMILARITY).
FT   BINDING      71     71       ATP (BY SIMILARITY).
FT   ACT_SITE    160    160       BY SIMILARITY.
FT   DOMAIN      318    337       CALMODULIN-BINDING (POTENTIAL).
FT   CONFLICT    278    280       VLD -> CFG (IN REF. 2).
FT   CONFLICT    302    302       N -> T (IN REF. 2).
SQ   SEQUENCE   469 AA;  52627 MW;  CE1F9867082F975 CRC64;

Query Match             37.6%;  Score 505;  DB 1;  Length 469;
Best Local Similarity   40.3%;  Pred. No. 9.7e-26;
Matches  108;  Conservative  50;  Mismatches  92;  Indels  18;  Gaps   5;

Qy      1 YDIGEELASSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVL 60
          || ||||| |:|||||:||:|  ::||  |||: | || || :||    |  |:| :||:
Db     42 FEVESELGRGATSIVYRCKQKGTQKPYALKVLKKT--------------VDKKIVRTEIGVLLRLS 93

Qy     61 HHNVITLHDVYENRTDVVHIIELVSGGELFDRLVQKESLSEEEATSFIKQILDGVNYLHT 120
          |:|:|  :::        :||||:|||||||  ||:|:|  || |  |:|:|| | ||
Db     94 HPNIIKLKEIFETPTEISLVLELVTGGELFDRIVEKGYYSERDAARDAVKQILEAVAYLHE 153

Qy    121 KKIAHFDLKPENIMLLDKNIPIPH--IKLIDGLAHEIEDGVEFKNIFGTPEFVAPEIVN 178
          |||||||||||||:|  |: ||     ||| |::|: | ||||:|||||||||||||:
Db    154 NGIVHRDLKPENLLYA---TPAPDALKIADPGLSKIVEHQVLMKTVCGTPGYCAPEILR 210

Qy    179 YEPLGLEADMWSIGVITYILLSGASPFL---GDTKQETLANITSVSYDFDEEFFSHTSEL 235
          | |    | || |:| |||::||| |      |:  |  | ||||:  |||| ::|:|
Db    211 GCAYGPEVDMWSVGIITYILLCGFEPPYDERGD--QFMFRRILNCEYYFISPWWDEVSLN 268

Qy    236 AKDFIRKLLVKETRKRLTIQEALRHPWI 263
          |||:|:||||:|  |||| ||||:|||:
Db    269 AKDLVKKLIVLDPKKRLTTFQALQHPWV 296

Search completed: May 18, 2002, 05:12:37
Job time: 1438 sec

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